

The predicted protein sequences of CssI (A), Hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A (F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

BEST AVAILABLE COPY

A
 MLASFQFCILPRTYRTLLCSAGAGPLLIQFVTVASALALAPTAVVARQGAAAFVTVNSIDVCPKKVAQEIIINPGPKVVTTP
 YTCDQVKLGHLDSYNNFDFIEPLTKDTFPYCKALKVFDNEGCLGFPTLWIPLESPLIEDKC1PEHYFSDEVKSISFQLDCRE
 DAPVKKEPYGPKEGAEQSAPQAHEHSTKQDQQGSHQGQEVCQNSPKQEARQGSRPAAAPKQEQEAEQASEAAPEKKASNPAD
 SLGLGEELTKVLGFR

B
 VRFPVPDDITVKQATEKCGDQAQLSCCNKATYAGDVTDIDEGLAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
 DLVNQKCKQNIACCQNSPDAVRFP

C
 MATPKVGINGFGRIGRIVGLNSLHGVDVVAVNDPFIEVHYAAYMLKYDTTHGQFKTIETYDQGLIVNGKKIRFYAEKD
 PSQIPWSETGAAYIVESTGVFTTKEKASAHLKGGAKKVIISAPSADAPMFVMGVNNNTTYTSDIQLSNASCTTNCLAPLA
 KVINDKFGIVEGLMTTVHSYATQKVVDAPSNDWRRGGRTAAQNIIPSTGAAKAVGVKVIPSLNGKLTGMAMRPTSNVS
 VVDLTCRLEKGASYDEIKQAIKAASEEGELKNILGYTEDDVVSSDLNGDERSSIFDAKAGISLNPNFVKLVAYDNEW

D
 MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGKGVLKAVKNVNETIGPALIKENI
 DVKDQSKVDEFLNKLDGTANKS NLGANAILGVSLAVAKAGAAEKGVPLYAHISDLAGTKKPVLPVPFQNVLNGGSHAGGR
 AFQEFMIVPDSAPSFSSEALRQGAEVYQKLKALAKKKYQGSAGNVGDEGGVAPDQIQTAAEALDLITEAEIQAGYTGK
 IKIAMDVASSSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAKYPIVSIEDPFAEDDWEAWSYFYKTSDFQIVGD
 DLTVTNPGRRIKKAIELKSCNALLKVNQIGTLTESIQAAKDSYADNWGMVMSHRSGETEDVTIADIAVGLRSGQIKTGAPCR
 SERLAKLNQILRIEEELGENTVYAGSKFR TAVNL

E
 MRLTFIPSLIGVANAVCPYMTGELNRRDEISDGAAAATEEFLSQYYLNDNDAFMTSDVGGPIEDQNSLSAGERGPTLLED
 IFRQKIQRFDHERVPERAVERHARGAGAHGVFTSYGDFSNITAASFLAKEGKQT PVFVRESTDVAGSRGSSDLARDVHGFA
 TDEGNDF DIVGNNI PVFFIQDAILFPDLIHAVKPRGDNEIPQAATAHDSAWDFFSQQPSMHTLLWAMSGHGI PRSF
 RHVDGFVGHTFRFVTDGASKLVKFWKSLQGKASMWEEAQQTSGKVPDFMRQDLHDAIEAGRYPEWELGVQIMDEEDQLR
 FGFDLLDPTKIVPEEFVPIKLGKMQLNPNRNYFAETEIQVMFQPGHIVRGVDFTEDPLLQGRLFSYLDTQLNRHGGPNFEQ
 LPINQPRVPVHNNDGAGQMFIPLNPHAYS PTKTSVNGSPKQANQTVGDGFTTAPGRRTSGKLVRAVSSSFEDVWS
 QPRLFYNSLVPAAKQFVIDAIRFENANVKSPVKKNNVIIQLNRIDNDLARRVARAIGVAEPEPDPTFYHNNKTADVGTG
 TFKLKKLDGLKVGVLSVQHPGSVEASTLRDRLKDDGVVVAERLADGVDTQYSTS DAIQFDAVVVAAGAESLFAASSFTGG
 SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQS VTDFFANDLKEGLRTFKF
 LDRFPVDH

F
 MATKIAAGGLHRAOEVLQNTSSSKKLV DLERDTADAHTOQPLTTDHGVRVSNTDQWLRTVNDRTGPSLLEDQIAREKIH
 DHERI PERVVHARGTGAFGNFKLKESIEDLTYAGVLTDTSRNTPVFRSTVQGSRGSA DTVDVRGFAVKFYTD
 EGNWDIV GNNIPVFFIQDAVKFPDFVHAVKPEPHNEVPQAAQTAHNNFWDFVYLHPEATHMFMWAMS DRAIPRSYRMMQGFGVN
 TFA LVNKEGKRHFVFKFWIPLGVHSLVWDEALKLGQDPDFHRLKDLMEAIDNKAYPKWDFAIQVIEEKQDDFEFDILD
 DAT KIWPENLVPLRVIGELELNRNVDEFFPQTEQVAFCTSHIVPGIDFTDDPLLQGRNF SYDTQISRLGINWEELPINR
 PCPV LNHNRDGQMRHRITQCTVNYWPNRFEAVPPTGKGSVGGFTTYPQRVEGIKRNRAINDKFREHHNQAQLFYNSMS
 EHEKLHMKA KAFSCHCDDPTVYERLAGHLAEIDL ELAQKVAEMVGAPI PAKLQNHGRRA PHLSQTEFIPKNPTIASR
 RIAI IGDGYDPVASTGLKTAIAASALPFIIGTKRSIAYATEDKTSKGII PDPHYDGQRSTMDATFIPGGPHVATL
 RQN GQTKYWISETFGHILKALGATGEAVDLVKETLSGTLHVQASSQSPPEPVWYGVVTAGGKQKPEFKE SVQILKGAT
 DFVGKFFYQISQHNRNYQRELDGLASTIAF

G
 MVTYNTILVLPGDGIGPEVMTEAVKVLKV FENEHRKFNLRQELIGGC SIDA HGKSVT EEVKKALES DAVLFAAVGGPKW
 DHIRRG LDGPEGGLLQLRKAMDIYANLRPCSASSPSASI AKEFSPF RQEVIEGVDFVVREN CGGAYFGKKIEEEDYAMD
 EWGYSER EIQ RITRLX₁AEX₂ ALRHNP PWPVISLDKANV LASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATN
 PRALN GVILADNTFGDMISDQAGSIVGTLGVLP SASLDGLPSETRKRTNGLYEP THGSA PTIAGQNTIANPVAMILCV ALMFY SLD
 MTEA QRIEKAVQVLDAGIRTPDLGGKSGTNEVGDAIV AALQGSS

FIGURE 1

The predicted antigenicity indices of CssI (A) and hydrophobin (B) reisdues.

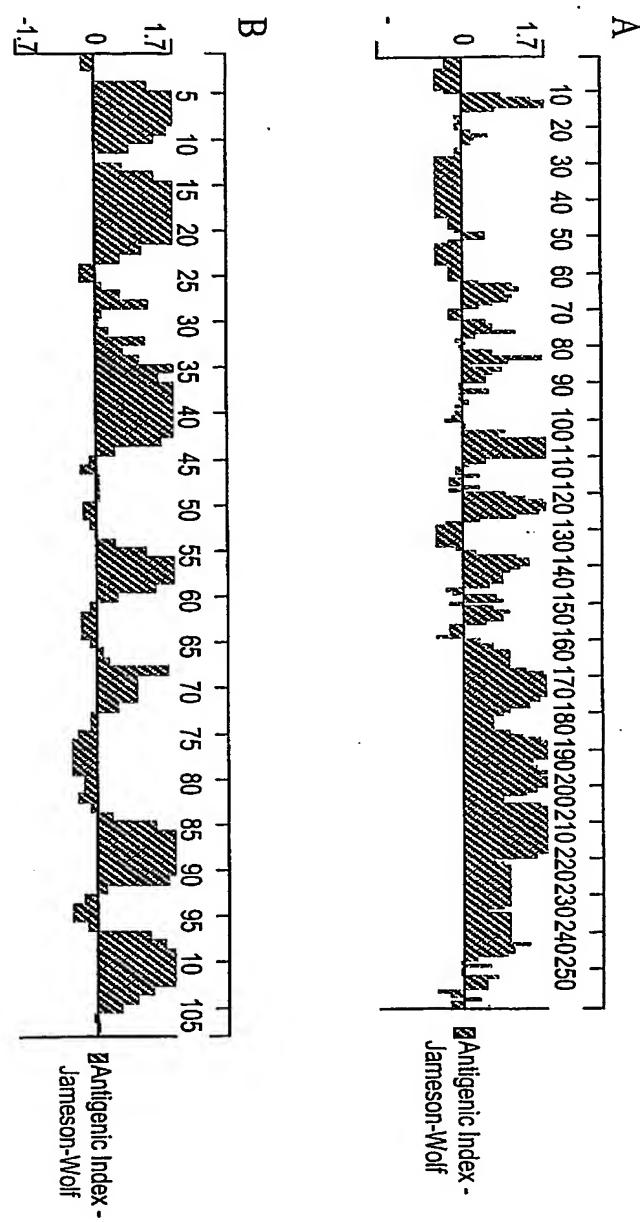


FIGURE 2

Alignment of the predicted protein sequences for GAPDH-A (AfA), GAPDH-B (AfB) and GAPDH-C (AfC).

FIGURE 3

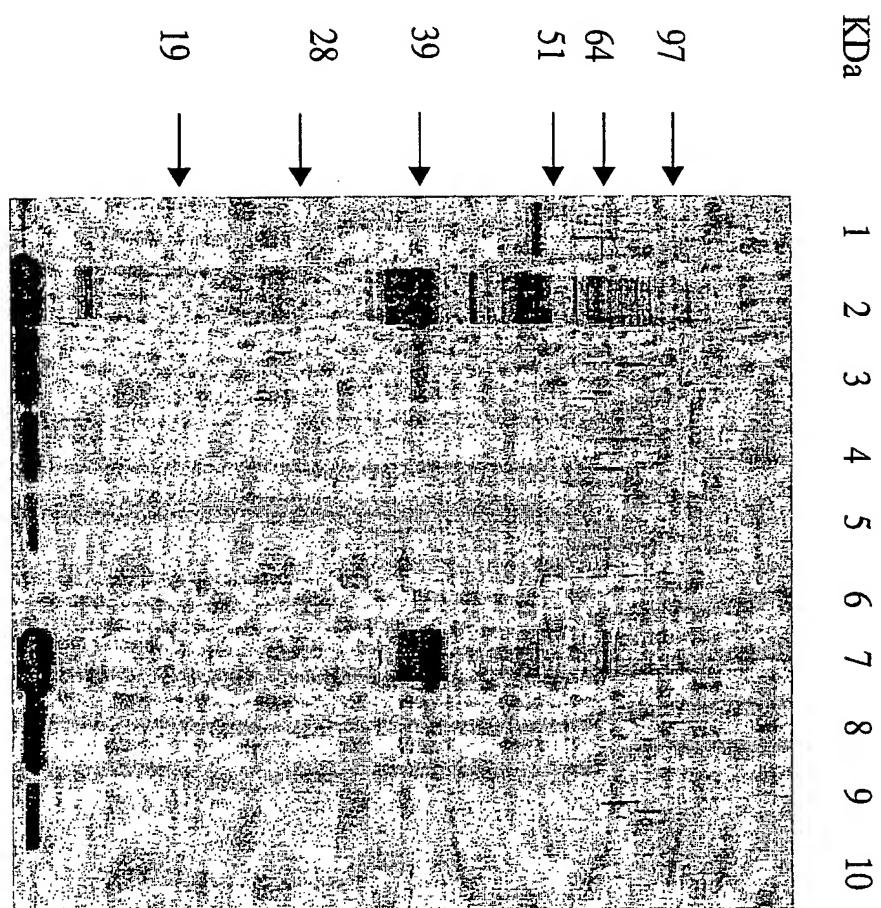


FIGURE 4

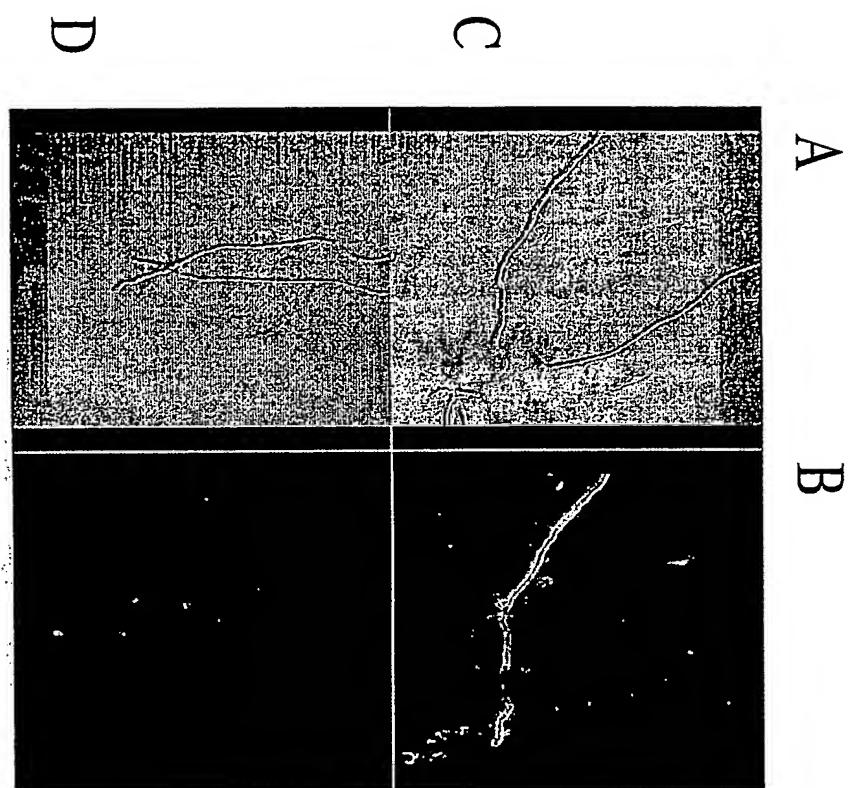


FIGURE 5

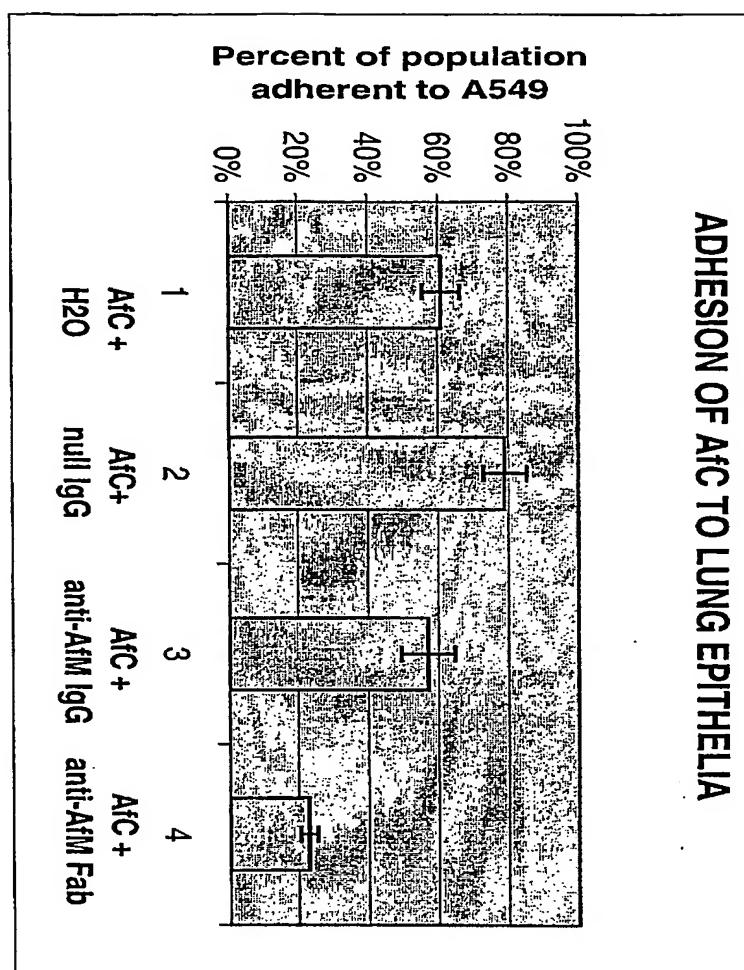


FIGURE 6

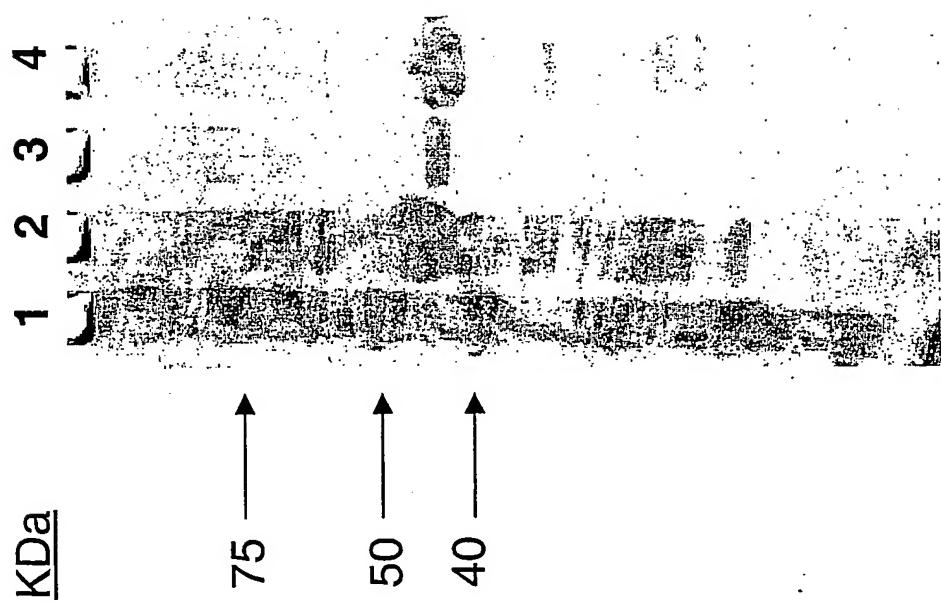


FIGURE 7

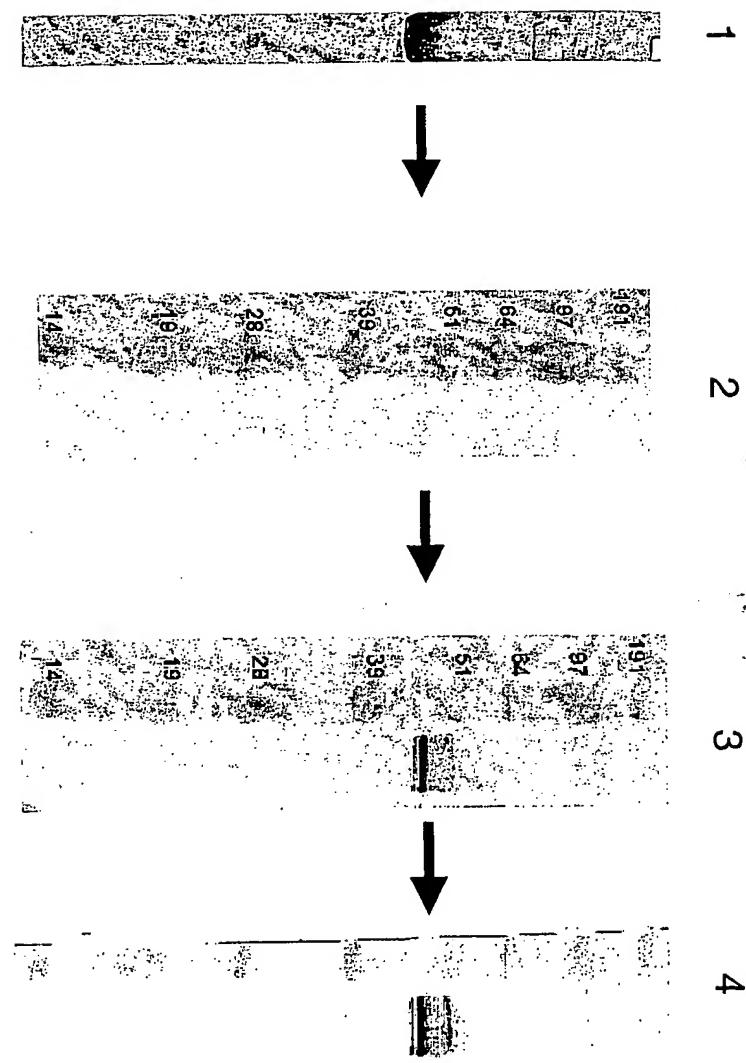


FIGURE 8

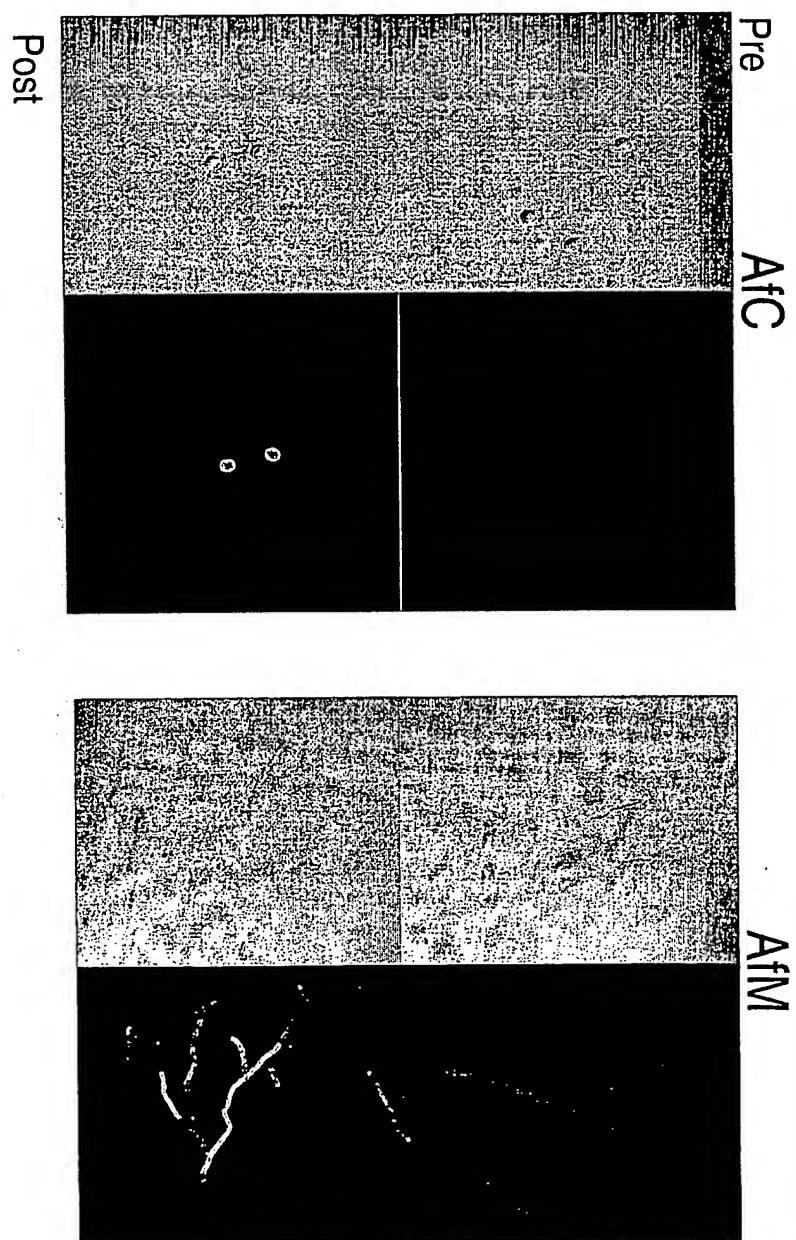


FIGURE 9

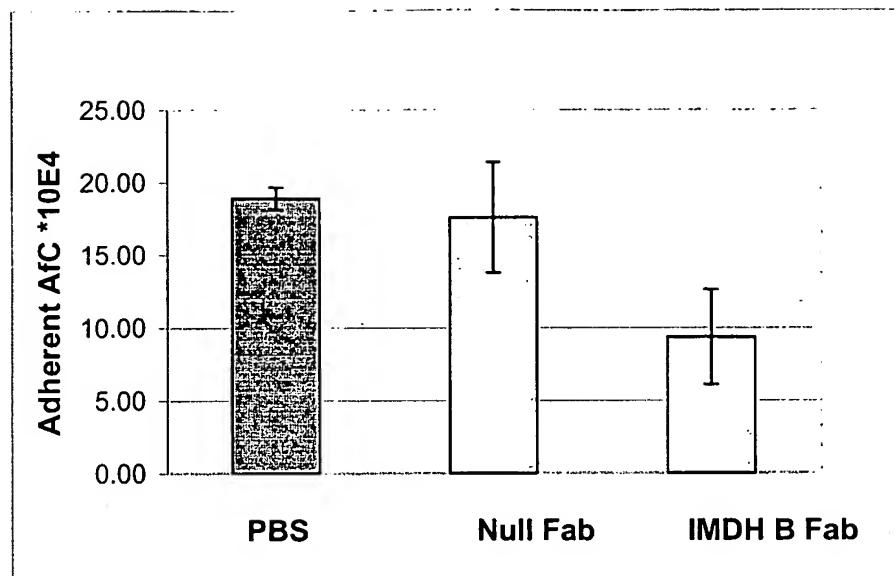


FIGURE 10

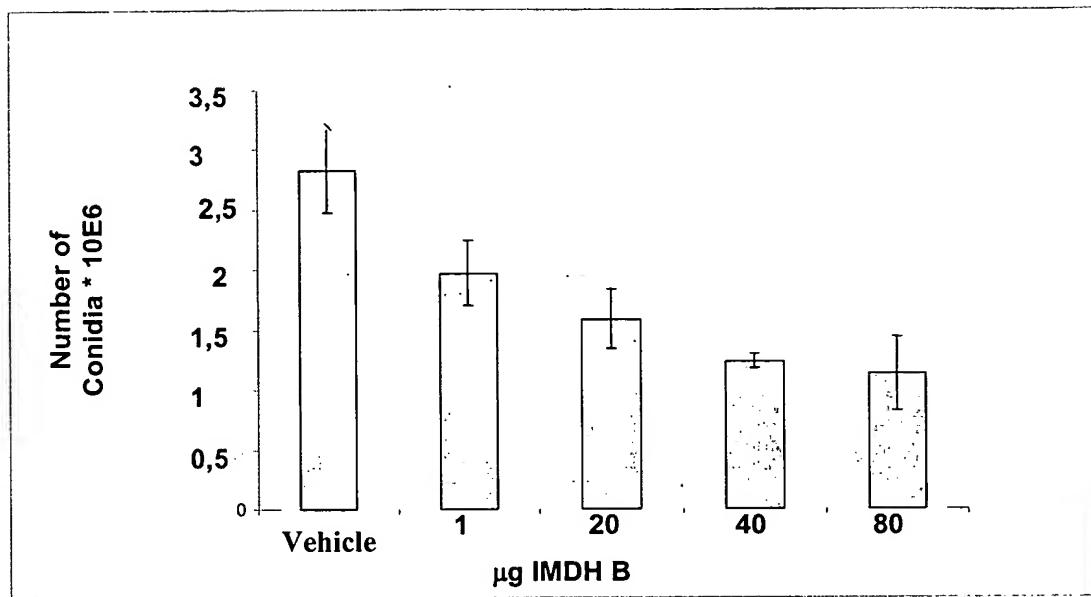


FIGURE 11

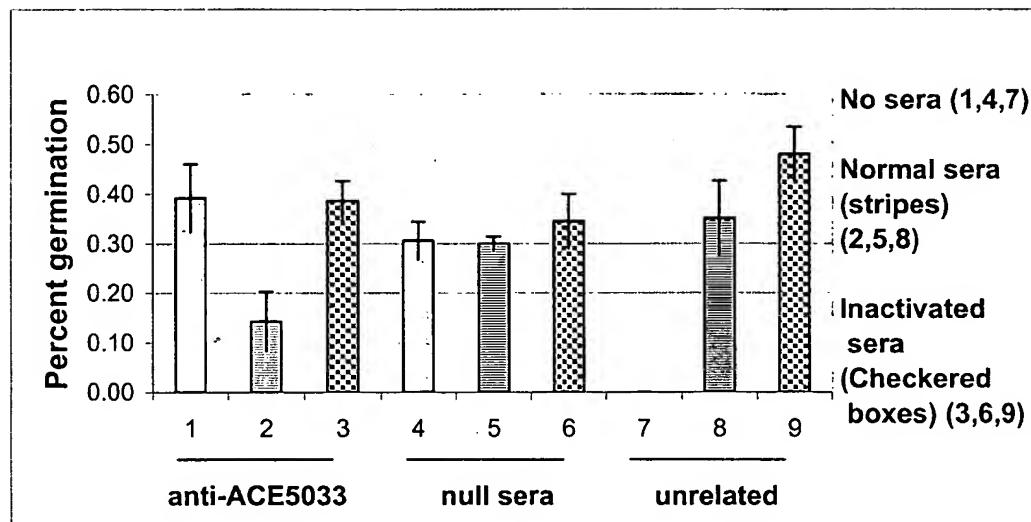


FIGURE 12

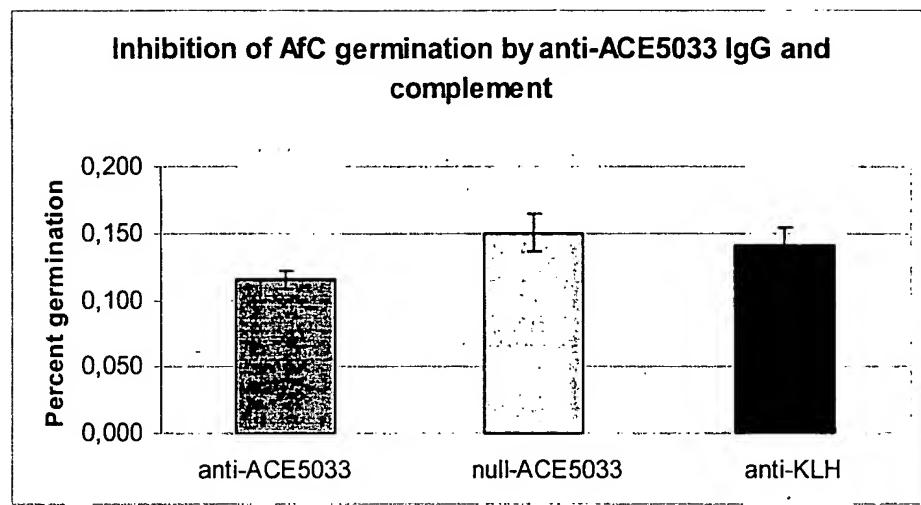


FIGURE 13

IMDHB1: 3 SYNIVVFAGDHCGPEVSS----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
 +YNI+V GD GPEV + VL+V E + FNL+ +L+GG S IDA G +T+E
 IMDHB2: 4 TYNILVLPGDGIGPEVMTEAVKVLKFEN--EHRKFNLRQELIGGCS-IDAHGKSVTEEV 60

 IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRLRKEMGTFGNLRPCNFAAPSLV-- 113
 AA +DAVL A+GGPKW G PE GLL+LRK M + NLRPC+ ++PS
 IMDHB2: 61 KKAALESDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSASIA 120

 IMDHB1: 114 -DGSPLRPEVCRGVDFNIIRELTGGIYFGDRKEDDGSGFAMDTEPYRSRAEIERITRLAAH 172
 + SP R EV GVDF ++RE GG YFG + E++ +AMD YS EI+RITRL+A
 IMDHB2: 121 KEFSPFRQEVIEWGVDFVVVRENCGGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178

 IMDHB1: 173 LALQHNPPPLPVWSLDKANVLATSRLWRKTVTEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
 +AL+HNPP PV SLDKANVLA+SRLWR+ V + M E+PO+K+ HOL DSA++I+ PR
 IMDHB2: 179 IALRHNPWPVISLDKANVLAASSRLWRRVVEKMTTEYQPVKLVHQLADSASLILATNPR 238

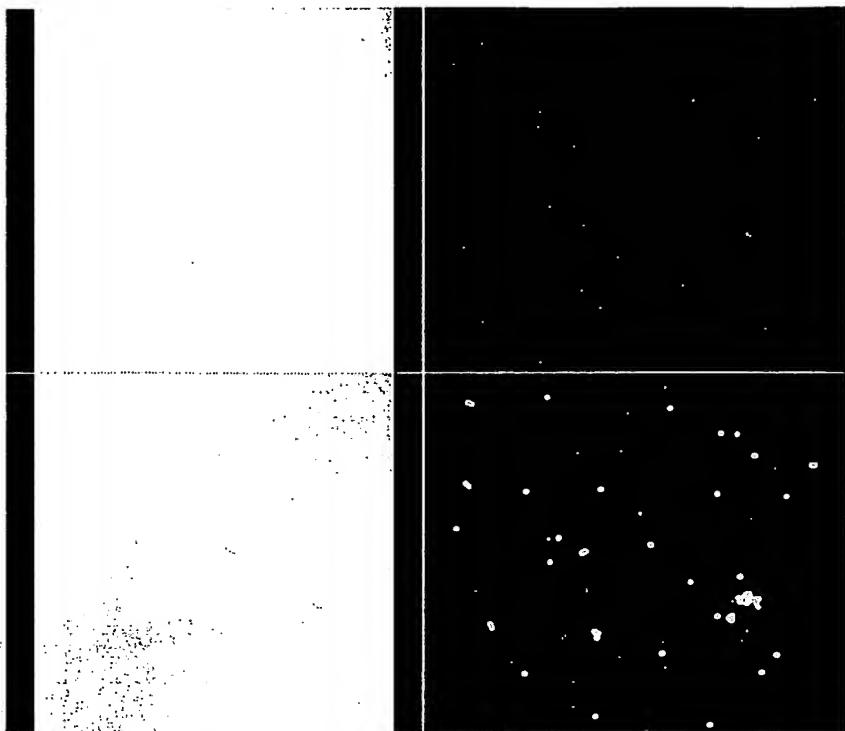
 IMDHB1: 233 KLNGIVVTSNLFGDIISDEASVIPHGSAPDI 291
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + + NG+YEP HGSAP I
 IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPTHGSAPTI 298

 IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARAIETAVRNIEAGIRTADIGGKSTTSEVGD 351
 AG+ I NPVA IL VA+M +YSL+ +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
 IMDHB2: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRT PDLGGKSGTNEVGD 358

 IMDHB1: 352 AVAAELE 358
 A+ A L+
 IMDHB2: 359 AIVAALQ 365

FIGURE 14

AfC



AfM

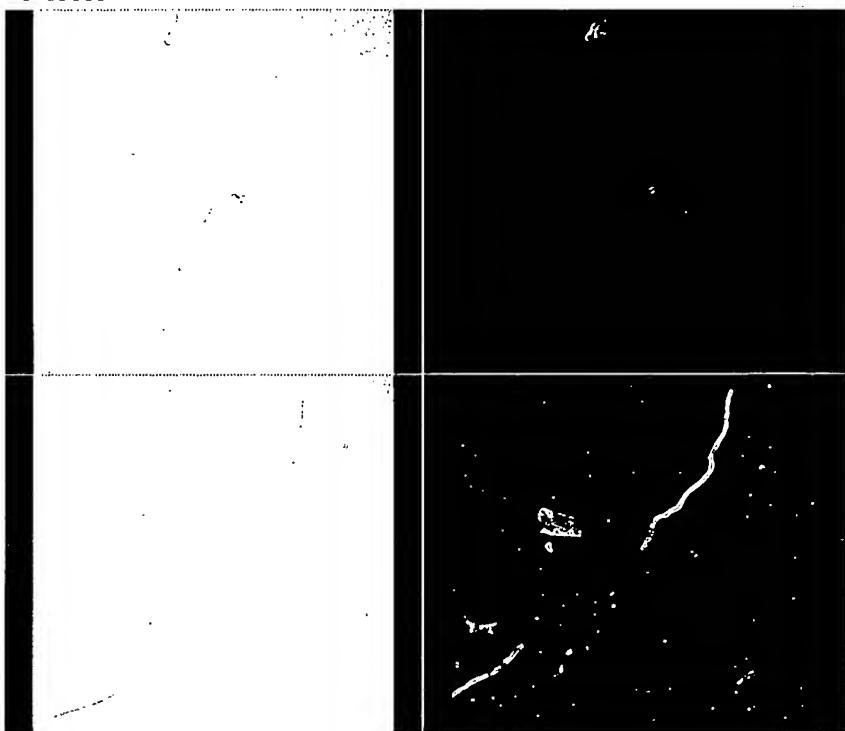


FIGURE 15

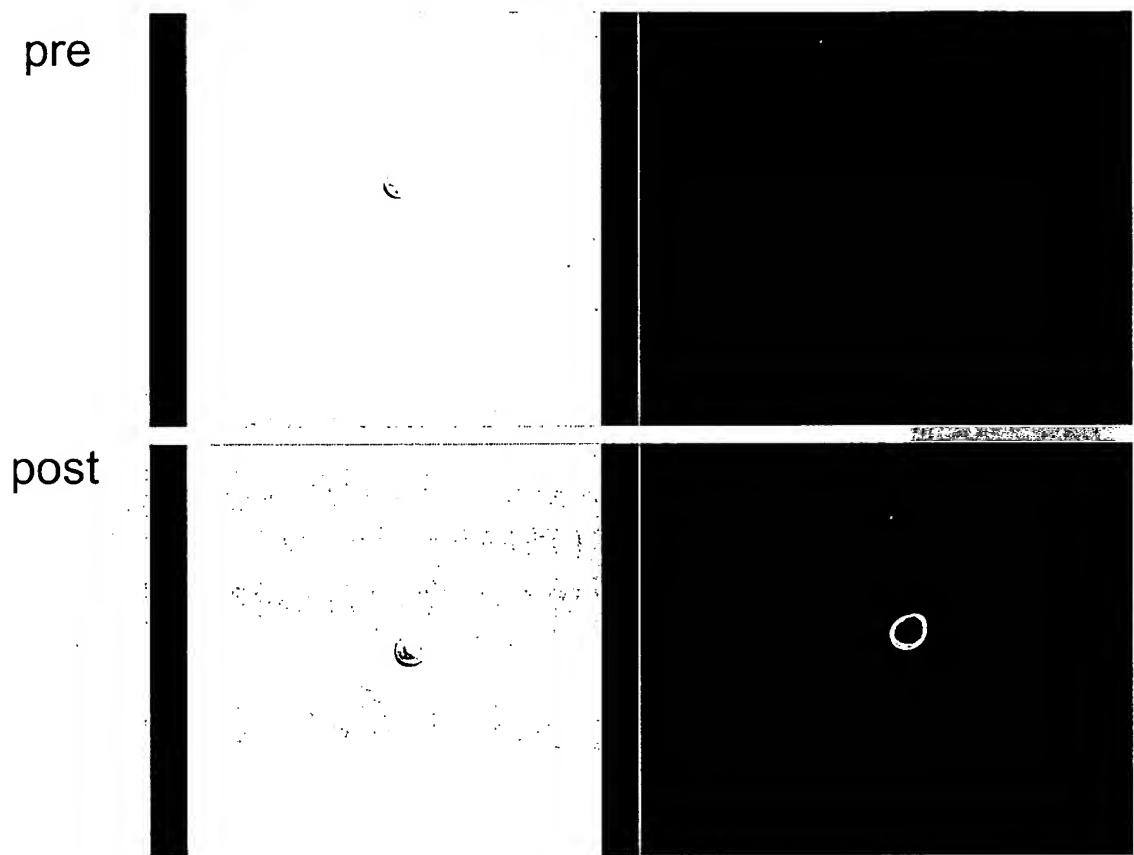


FIGURE 16

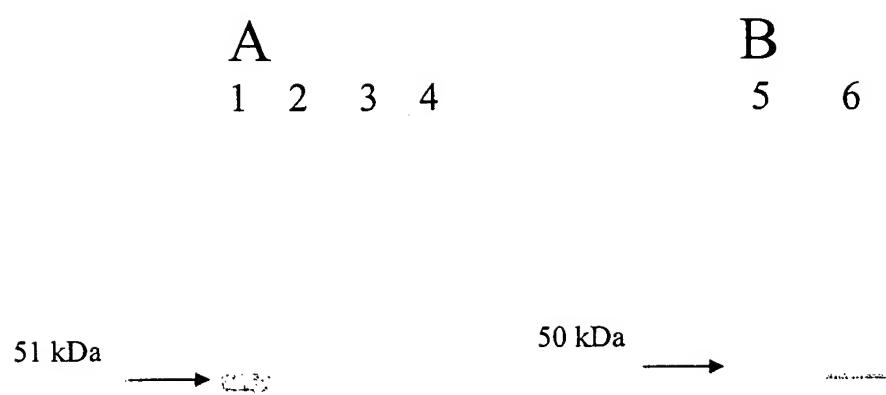


FIGURE 17

BLAST OF SEQ ID NO:36 AGAINST:

Candida orf:

>orf19_7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
 Length = 1122

Score = 335 bits (860), Expect = 1e-92
 Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)
 Frame = +1

Query: 2 VTTYNILVLPGDGIGPEVMTEAVKVLVFEN----EHRKFNLRQEELIGGCSIDAHGKSVT 57
 V T I VLPGD +G E++ EA+KVLK E + +F+ + LIGG +IDA G +
 Sbjct: 7 VKTKTITVLPGDHVGTIEVNEAIKVLKAIEAATPYQKIQFDFKHHHLIGGAAIDATGVPLP 186

Query: 58 EEVKKALESDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
 ++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
 Sbjct: 187 DDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEEEDY----AMDEWGYSEREIQRI 172
 E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
 Sbjct: 358 L---ELSPLKAEVVKGTNLIIVRELVGGIYFGERQEQQEESDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPWPVISLDKANVASSRLWRRVVEKTMTEYQPQVKLVHQLADSASLI 232
 TR++A +AL+HNPP P+ SLDKANVASSRLWR+ V+K ++ E+P + + HQL DSA++I
 Sbjct: 529 TRMAAFMALQHNPLPWIWSLDKANVASSRLWRKVISEEFPALSVQHQLIDSAAMI 708

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPTH 292
 L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
 Sbjct: 709 LIQNPPTKLNGIIITSNMFQDIISDEASVIPGSLGLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
 GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
 Sbjct: 883 GSAPDLPA-NKVNPPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTADLRGTSS
 1059

Query: 353 TNEVGDAI 360
 T EVGDAI
 Sbjct: 1060TTEVGDAI 1083

Candida seq orf10262:179916-178795 1
 VKTKTITVLPGDHVGTIEVNEAIKVLKAIEAATPYQKIQFDFKHHHLIGGAAIDATGVPLPDDALESAKS
 SDAVLLGAVGGPKWGTGTVRPEQGLLKIRKELNLYANIRPCNFASDSLLELSPLKAEVVKGTNLIIVRE
 LVGGIYFGERQEQQEESDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPLPWIWSLDKANVASSRLWR
 KTVDKVISEEFPALSVQHQLIDSAAMILIQNPTKLNGIIITSNMFQDIISDEASVIPGSLGLPSASLA
 SLPDTNTAFGLYEPCHGSAPDLPANKVNPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTAD
 LRGTSS1060TTEVGDAI

BLAST OF SEQ ID NO:36 AGAINST:

Elrond pep

A. nidulans

>AnrP4374925 LE3B _ ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM
dehyd
Length = 370

Score = 597 bits (1540), Expect = e-171
Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPGDGIGPEVMTEAVKVLKFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKA 63
+YNILVLPGDGIGPEVM EA K+L +F +F + ELIGGCSID HGKSVT+ V A
Sbjct: 5 SYNILVLPGDGIGPEVMAEATKILSLFNTSTVRFRQTELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLEDGPEGGLLQLRKAMDIYANLRPCSASSPSASIAKEF 123
A+ SDAVLFAAVGGPKWDHIRRGLEDGPEGGLLQ+RKAMDIYANLRPCS SPS IA++F
Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLEDGPEGGLLQVRKAMDIYANLRPCSDSPSREIARDF 124

Query: 124 SPFRQEVIEGVDFVVVRENCGGAYFGKKIEEEDYAMDEWGYSERIQRITRLSAEIALRH 183
SPFRQ+VIEGVDFVVVRENCGGAYFGKK+EE+DYAMDEWGY S EIQRITRLSAE+ALRH
Sbjct: 125 SPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSAEIQRITRLSAEALRH 184

Query: 184 NPPWPVISLDKANVLASSRLWRRVVEKTMTEYQPQVKLVHQLADSASLILATNPRLNGV 243
+PPWPVISLDKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNPRLNGV
Sbjct: 185 DPPWPVISLDKANVLASSRLWRRVVEKTMSEEYPQVKLVHQLADSASLIMATNPRLNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSE-TRKRTNGLYEPHTGSAPTIAGQN 302
ILADNTFGDM+SDQAGS+VGTLGVLPASLDGLP +++ +GLYEPHTGSAPTIAG+N
Sbjct: 245 ILADNTFGDMVSQAGSLVGTGVLPASLDGLPKPGEQRKVHGLYEPHTGSAPTIAGKN 304

Query: 303 IANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRT PDLGGKSGTNEVGDAIVA 362
IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
AL+G
Sbjct: 365 ALKG 368

>AnrP4374925 niger seq
MSEKSYNILVLPGDGIGPEVMAEATKILSLFNTSTVRFRQTELIGGCSIDTHGKSVTQA
VLDAAVSSDAVLFAAVGGPKWDHIRRGLEDGPEGGLLQVRKAMDIYANLRPCSDSPSREI
ARDFSPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSAEIQRITRLSAEL
ALRHDPWPVISLDKANVLASSRLWRRVVEKTMSEEYPQVKLVHQLADSASLIMATNPRA
LNGVILADNTFGDMVSQAGSLVGTGVLPASLDGLPKPGEQRKVHGLYEPHTGSAPTI
AGKNIANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGD
AVVAALKGEL

FIGURE 19

BLAST OF SEQ ID NO:36 AGAINST:

BLASTP:temp job2 pep 6 AnrP3711474
>AnrP3711474 hypothetical protein [Aspergillus oryzae]
 Length = 364

Score = 375 bits (963), Expect = e-104
 Identities = 195/367 (53%), Positives = 260/367 (70%), Gaps = 10/367 (2%)

Query: 2 VTTYNILVLPGDGIGPEVMTEAVKVLKVFE-NEHRKFNLRQE^LIGGCSIDAHGKSVTEEV 60
 +++YNI+V GD GPEV EA+KVL+ E N FNL+ L+GG SIDA G +T+E
 Sbjct: 1 MSSYNIVVFGGDHCGPEV^TAEAIKVLR^AVEKNRDVT^NLQDHLLGGASIDATGSPLTDEA 60

Query: 61 KKAAL^ESDAVLFAAVGGPKWDH^IRRLDGPEG^GLLQLRKAMDIYANL^RPCSASSPSASIA 120
 AA +DAVL A+GGPKW G PE G+L+LRK M + NLRPC+ ++PS
 Sbjct: 61 LNAAKNADAVLLGAIGGP^KWG---TGAVRPEQGILKLR^KEMGT^FGNL^RPCNFAAPSLV-- 115

Query: 121 KEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEEED--YAMDEWGYSEREIQRITRLSAE 178
 E SP R +V GV+F ++RE GG YFG++ E++ YAMD YS EI+RI RL+A
 Sbjct: 116 -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGS^GYAMDTEPYSRAEIERIIRLAAH 174

Query: 179 IALRHNP^PWPV^ISLDKANV^LASSRLW^RRV^VEKT^MTEY^PQV^KL^VHQLADSASL^LILATNPR 238
 +AL+H+PP PV SLDKANVLA+SRLWR+VV + M E+PQ+K+ HQL DSA++I+ NPR
 Sbjct: 175 LALQHD^PPLPVWSLDKANV^LAT^SR^LWRKV^VTEV^MAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239 ALNGVILADNTF^GDMISDQAGSIVGTLGV^LPSASLDGLPSETRKRTNGLYE^PTHGSAP^I 298
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + NG+YEP HGSAP I
 Sbjct: 235 QLNGIVVTSNLFGDIISDEASV^IPG^SGL^LPSASLSGIP-DGNSKVNGIYEPIHGSAPDI 293

Query: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRT^PD^LGGKSGTNEVGD 358
 AG+ I NPVA IL VA+M +YS + EA+ IE+AV V++G+RT D+GGK+ T EVGD
 Sbjct: 294 AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDI^GGGKATTAEVGD 353

Query: 359 AIVAALQ 365
 A+ A L+
 Sbjct: 354 AVAAELE 360

Oryzae seq >AnrP3711474
 MSSYNIVVFGGDHCGPEV^TAEAIKVLR^AVEKNRDVT^NLQDHLLGGASIDATGSPLTDEA
 LNAAKNADAVLLGAIGGP^KWG---TGAVRPEQGILKLR^KEMGT^FGNL^RPCNFAAPSLVESSPL
 RADVCRGVNFNIIRELTGGIYFGERKEDDGS^GYAMDTEPYSRAEIERIIRLAAH^LALQHD
 PPLPVWSLDKANV^LAT^SR^LWRKV^VTEV^MAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
 VTSNLFGDIISDEASV^IPG^SGL^LPSASLSGIPDGN^SKVNGIYEPIHGSAPDIAGKGIVN
 PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDI^GGGKATTAEVGD^AVAELE
 KLLK

FIGURE 20

BLAST OF SEQ ID NO:36 AGAINST:

BLASTP:temp job2 pep 9 AnrP4379986
 >AnrP4379986 conserved hypothetical protein [Aspergillus **nidulans**
 FGSC A4
 Length = 357

Score = 149 bits (376), Expect = 1e-36
 Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1 MVTTYNILVLPGDGIGPEVMTEAVKVLKFENEHRKFNLRQEELIGGCS--IDAHGKSVTE 58
 M TY I +P DGIGPEV+ V VLK ++ + F+L + S A GK ++
 Sbjct: 1 MAKTYRIATIPADGIGPEVIDAGVIVLKLADKLQSFSLDFTHLDWSSETFKATGKYIPD 60

Query: 59 EVKKALESDAVLFAAVGGPKW-DHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
 + ++DA+LF AVG P DHI G L + + YAN+R P+
 Sbjct: 61 GGLEVKKNDAILFGAVGAPDVPDHISLW-----GLRLAICQPFQQYANVR-----PTR 109

Query: 118 SIAKEFSPFRQEVEIGVDFVVVRENCGGAYFGK----KIEEEDYAMDEWGYSEREIQRI 172
 + SP R+ +D+V+VREN G Y G+ + + A + +S + ++RI
 Sbjct: 110 VLRGTQSPLRKCNTGLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERI 169

Query: 173 TRLSAEIALRHNPWPVISLDKANVLASSRLWRRVVEKTMTEYPOVQLVHQLADSASLI 232
 R + E A + P + + K+N + + V + ++P+V + L D+ +
 Sbjct: 170 MRFAFETAAK-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTR 228

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPTH 292
 + P +L+ I+A N D++SD A ++ G++G+ P+++LD ++ ++EP H
 Sbjct: 229 MVLKPESLD-TIVASNLHADILSDLAAALAGSIGIAPTSNLD-----PTRQNPSMFEPIH 282

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEQRRIKAVQGVLDAGIRTPDLGGKSG 352
 GSA I G+ IANPVA A M + L + A ++ + V+ V ++GI T DLGG +
 Sbjct: 283 GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCVESVCESGILTADLGGTAT 341

Query: 353 TNEVGDAIV 361
 T EV A+V
 Sbjct: 342 TKEVTSAVV 350

Nidulans seq >AnrP4379986
 MAKTYRIATIPADGIGPEVIDAGVIVLKLADKLQSFSLDFTHLDWSSETFKATGKYIPD
 GGLEVKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQQYANVRPTRVLRGTQSPLRK
 CNTGLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETAAKR
 PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTRMVLKPESLDTIV
 ASNLHADILSDLAAALAGSIGIAPTSNLDPTRQNPSMFEPIHGSADFITGKGIANPVATF
 WTAEMLEWLGEKDAADKLMQCVESVCESGILTADLGGTATTKEVTSAVVEEINRLN

FIGURE 21

BLAST OF SEQ ID NO:36 AGAINST:

>gnl|TIGR 222929|contig:1772:c posadasii Coccidioides posadasii C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128
 Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)
 Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPPWPVISLDKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVRQRIARLAHVALRHDPPWPVISMDKANVLASSRLWRRVVEKLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRVLNGVILADNTFGDMLSDQAGSLIGTLGVLPASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPSASL G+P
 Sbjct: 33626 QVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPETHGSAPT-----IAGKNIANPTAMILC 315
 + + + K LYEPETHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGGKSYALYEPETHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFRYSFNMEEARQIEDAVRAVLDRLGLRTPDGLGGNSSTQEFGDAVVAALQ 368
 V++MFRYSFNME EA+ IE+AV A L+ G+RTPDGLG + T + G+A+VA ++
 Sbjct: 33266 VAMMFYRYSFNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK 33108

Query: 4 TRAYNILVLPGDGIGPEVMAEAIKVLRTFNSSSMQFHLQEELIGGISIDTHGHSVTQPXX 63
 ++ YNIL LPGDGIGPE+MAEAIKVL+ F+S ++ F+I+ ELIGG S+D HG +T
 Sbjct: 34383 SKTYNILTLPGDGIGPEIMAEAIKVLQAFSSPNLFNLRNELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGGSKVDHIRRGLDGPEGGLLQVRKAMDIYANLRPCSDVPSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALESDAVLFASVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVRPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVEIGVDFVVVRENCGGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVV+RENCGGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVLRENCGGAYFGKXVEDEDY 33919

Coccidioides 2

SKTYNILTLPGDGIGPEIMAEAIKVLQAFSSPNLFNLRNELIGGCSIDAHGTPITDAVKQAALESDAVLF
 ASVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVRPCSTDVCAVSREFSPYRTEVVEGVDFVVL
 ENCGGAYFGKXVEDEDYAMDEWGYSTQEVRQRIARLAHVALRHDPPWPVISMDKANVLASSRLWR
 RVVEKLTTEFPQVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLS
 GIPGEKRKDGGKSYALYEPETHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILCVAMM
 FRYSFNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK

SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.C11
 (289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
 Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

Query: 148 FGKKIE--EEDYAMDEWGYSEREIQRITRLSAEIALRHNPWPVISLDKANVLASSRLWR 205
 FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DKANVLA+SRLWR
 Sbjct: 173334 FGERQETNDEGVAVDQCIYSKPEIERITRVAQQIAALAAEPPPLPITSVDKANVLATSRLWR 173513

Query: 206 RVVEKTMTEYPOVKLVHQLADSASLILATNPRLNGVILADNTFGDM----- 253
 + V + M EYPQ+KL HQL DSA++I+ NNP LNGV+L +N FGDM
 Sbjct: 173514 KTVSELMAREKEYPQLKLEHQQLVDSAAMIMIANPRKLNGVLLTENMFGDM*VLSMVTKYRC* 173693

Query: 254 -----ISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
 S A + L + P LP ++ HGS
 Sbjct: 173694 VCVVFLTKAPSSPAPLVSSLLRLSPVPPTLSLPPVMSRTSISFPFLTYPN*PLCSIHGS 173873

Query: 295 APIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
 AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
 Sbjct: 173874 APDIAGQGIANPIGTLISAAMMLRYSLGKREAAALIEQAVQKVLDSEAESGGDYRTKDLG 174053

Query: 349 GKGSTNEVGDAAIVAAALQG 366
 G+ T EVGD +V L+G
 Sbjct: 174054 GQRSTKEVGDKVVVEVLKG 174107

Query: 15 IGPEVMTEAVKVLKFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
 IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
 Sbjct: 172844 IGPEVVAEAVRVLETIVNHSDLKLDLKSYDFGGAIDNHEGVPLPDETLKACKEADAVLMG 173023

Query: 74 A-----VGGPKWDHIRGLDGPEGGLLQLRKAMDIYANLRPCSASSPS 116
 A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
 Sbjct: 173024 ACDFLAIRIKS*TA*KGSVGGPKWGV--GPVRPEQGILKLRKELGLYANIRP--ANFAS 173188

Query: 117 ASIAKEFSPFRQEVIEGVDFVVVRENCGG 145
 S+ K SP +++ G D +V+RE GG
 Sbjct: 173189 ESSLKR-SPLKEDTARGTDIIVLRELLIGG 173272

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLPASLD-----GLPS---ETRKRTNGLYEPTH 292
 +L + +GD+SD + +G LG+ PS ++ G PS K ++E H
 Sbjct: 238292 LLIPHRYGDLSDLASAGLIGGLGLTPSGNIGKVSLSHDYGSPSIELTGDK*DASIFEAVH 238471

Query: 293 GSAPTIAGQNIANPVAMILCVALMFR----- 318
 GSAP I G+ +ANP A++L +M R
 Sbjct: 238472 GSAPDIEGKGLANPTALLSLLMMLR*VTQIPSIVPALYSPVDPDHTHPLARNVADLFVH 238651

Query: 319 YSLDMETEAQRIEKA--VQG-----VLDAGIRTPLGGKSGTNEVGD 358
 + + A +IEKA V G + + T DLGGK+GT E D
 Sbjct: 238652 RHMSLYELADKIEKAALSVSGTPWLFHTFEMLIQVS*TIAEGKAITRDLGGKAGTKEYTD 238831

Query: 359 AIVAAL 364
 AI++ L
 Sbjct: 238832 AILSKL 238849

Query: 95 LQLRKAMDIYANLRPCSASSPSASIAKEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEE 154
 L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
 Sbjct: 237609 LTLRRTFSILFANVRPC-----VSIKGYKTPY-----DNVNTVLIRENTGEYSG--IEH 237749

Query: 155 E 155
 E
 Sbjct: 237750 E 237752

Query: 5 YNILVLPGDGIGPEVMTEAVKVLK 28
 Y + ++PGDGIGPE+ ++ K
 Sbjct: 237256 YTVTLIPGDGIGPEIANSVKQIFK 237327

Query: 4 TYNILVLPGDGIG 16
 ++ I VLPGDGIG
 Sbjct: 172752 SFRITVLPGDGIG 172790

Clustalw of sequences of figure 18-22

```
! Sequence: BLASTP:temp job2 pep 4 AnrP4374925 nidulans (see figure 19)
! Sequence: BLASTP:temp job2 pep 6 AnrP3711474 oryzae (see figure 20)
! Sequence: BLASTP:temp job2 pep 9 AnrP4379986 nidulans (see figure 21)
! Sequence: USERPROTEIN:1 job6 1 candida (see figure 18)
! Sequence: USERPROTEIN:2 job7 2 coccidioides (see figure 22)
CLUSTAL W (1.82) multiple sequence alignment
```

temp_job2_pep_4_AnRP4374925	---SYNILVLPGDGIGPEVMAEATKILSLFNTST---
temp_job2_pep_6_AnRP3711474	-VRFRQTTELIGG
temp_job2_pep_9_AnRP4379986	-MSSYNIVVFGGDHCGPETVAAIKVLRAVEKNR---
1_job6_1	MAKTYRIATIPADGIGPEVIDAGVIVLKLADKLQS--
2_job7_2	-FSLDFTHLDWSS
	-VKTKTITVLPGDHVGTIEVNEAIKVLKIAEAATPYQKIQFDFKHHLIGG
	-SKTYNILTLPGDGIGPEIMAEAIKVLQAFSSPN---
	LNFnLRLNELIGG
	: * . : . * . * : . : * . . : .

temp_job2_pep_4_AnRP4374925	CSIDTHGKSVTQAVLDAVSSDAVLFAAVGGPKWDHIRRLDGPEGGLLQ
temp_job2_pep_6_AnRP3711474	ASIDATGSPLTDEALNAAKNADAVLLGAIGGPWKW---TGAVRPEQGLIK
temp_job2_pep_9_AnRP4379986	ETFKATGKYIPDGGLLEVKKNDAILFGAVGAPDVP---DHISLWGLRLA
1_job6_1	AAIDATGVPLPDDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGLLK
2_job7_2	CSIDAHGTPITDAVKQAALESDAVLFASVGGPKWDSSRRGLLEGPEGGLLQ

temp_job2_pep_4_AnRP4374925	YFG----KKVEEDDYAMDEWGYSAEIQRITRLSAELALRHDPWPVIS
temp_job2_pep_6_AnRP3711474	YFGERKEDDGSG---YAMDTEPYRSAEIERIIRLAALQHDPLPVWS
temp_job2_pep_9_AnRP4379986	YAGQGGGRSHRGHPWEVATEVAIFSRQGVVERIMRAFETAAKR-PRKLLTV
1_job6_1	YFGERQEQQESEDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPLPIWS
2_job7_2	YFG----KXVEDEDYAMDEWGYSTQEVQRIARLAAHVALRHDPWPVIS
	*** * : : : * * * : : * : * : : * : :

FIGURE 24

temp_job2_pep_4_AnRP4374925	LDKANVLASSRLWRRVVEKTMSEEYPQVKLVHQLADSASLIMATNPRALN
temp_job2_pep_6_AnRP3711474	LDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLN
temp_job2_pep_9_AnRP4379986	VTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTRMVLKPESLD
1_job6_1	LDKANVLASSRLWRKTVDKVISEEFPALSVQHQLIDSAAMILIQNPTKLN
2_job7_2	MDKANVLASSRLWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRSLN
	: *:*. .. : * : ::* :.. : * *: : : * *: :
temp_job2_pep_4_AnRP4374925	GVILADNTFGDMVSDQAGSLVGTGLVLPASLDGLP--KPGEQRKVHGLY
temp_job2_pep_6_AnRP3711474	GIVVTSNLFGDIISDEASVIPGSLGLPSASLSGIP---DGNSKVNGIY
temp_job2_pep_9_AnRP4379986	-TIVASNLHADILSDLAAALAGSIGIAPTSNLDPTR-----QNPMSMF
1_job6_1	GIIITSNMFGDIISDEASVIPGSLGLPSASLASLP---DTN-TAFGLY
2_job7_2	GVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIPGEKRKDGGKSYALY
	: :.* ..*: :** * . : * : *: * : :* ..:
temp_job2_pep_4_AnRP4374925	EPTHGSAPTIAGKNIANPTAMILCVALMFYSFNMEEARQIEAAVRTVL
temp_job2_pep_6_AnRP3711474	EPIHGSAPDIAGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVI
temp_job2_pep_9_AnRP4379986	EPIHGSAFDITGKGIANPVATFWTAAEMLEWLG-EKDAADKLMQCVESVC
1_job6_1	EPCHGSAPDL PAN-KVNPIATILSAASMLRLSLDCVKEAEALEEAVKQVL
2_job7_2	EPTHGSAPT-----
	*** ****
temp_job2_pep_4_AnRP4374925	DKGIRTSDLGGSTGTREFGDAVVAALKG
temp_job2_pep_6_AnRP3711474	ESGVRTGDIIGGKATTAEVGDAVAAELE-
temp_job2_pep_9_AnRP4379986	ESGILTADLGGTATTKEVTSAVV-----
1_job6_1	DSGIRTADLRGTSSTEVGDAI-----
2_job7_2	-----

FIGURE 25

Identification of peptides in AFC fractions.

Protein extract	CssI (AnrP440134)	Hydrophobin (AnrP5721)	GAPDH (AnrP53902)	Endoase (AnrP7789)	Catalases and IMDH B
Diffusate	KVAQETINPGPK	FPPFDITVK ATYAGDVTIDEGILAGTLK	AGISLNPNFVK TAQONIIPSSIGAK	NWNETIGPALIK VNGQIGLTTESTIQAK	Not detected
Cell surface exposed	VAQETINPGPK	FPPFDITVK ATYAGDVTIDEGILAGTLK	Not detected	Not detected	FGFDLIDPTK (Catalase B peptide AnrP977704) LX,AEX,AIR (IMDH B peptide)
Cell wall	KVAQETINPGPK VAQETINPGPK SISFQIDCR EGAEGSAPQAEHSTK WTTTPYTCDQVK	FPPFDITVK 3-12 ATYAGDVTIDEGILAGTLK 30-50 VPTFSNWSVVDLTCR YDPTHGQFK	AGISLNPNFVK TAQONIIPSSIGAK NILGYTEDDVSSDLNGDER	Not detected	TGRSLIADQIAR (Catalase A peptide AnrP14557)
Peptides used for Ab production	KVAQETINPGPKVWIT KEGANQSAQAEHSTK	PYPPDDITVKQATEKCGD ATYAGDVTIDEGIL	KVNNETIGPALIENID TSDFQIVGDDLTVINPGR	DEEDQQLRGFDLDPKIVP R1DNDLARRVARAIGV	

FIGURE 26

Biochemical characteristics of CssI.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isolelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

FIGURE 27

Sequence of Polypeptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins.

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTLIETYDQGLIVNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVVSSDLNGDERS (SEQ ID NO:11)	GAPDH B	+++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTDIPEGIL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEEDQLRFFGFDLLDPPTKIVP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETIGPALKEND (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFQIVGDDLTVTNPGR (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQQSAQPAEHSTK (SEQ ID NO:8)	CssI	+++	+++
Peptide 1	KVAQEINPGPKWTT (SEQ ID NO:7)	CssI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

FIGURE 28

Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	<u>Anti IMDH-B intensity</u>	
			<u>Conidia</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergillosis	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

FIGURE 29

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